

Amendments to the Specification:

Please insert the following table at line 25, page 23 of the specification:

TABLE 1

RNA fragment No	nucleotides	K _d _{app} (in nM)
1, <u>SEQ. ID NO.15</u>	UUUUUUUUU	not bound
2, <u>SEQ. ID NO.16</u>	UUUUUUUUUU	0.97 +/- 0.19
3, <u>SEQ. ID NO.17</u>	(AUUU) ₂ A	not bound
4a, <u>SEQ. ID NO.18</u>	(AUUU) ₃ A	1.40 +/- 0.39
4a, <u>SEQ. ID NO.19</u>	AUUUAUUUAUUUA	not bound
4b, <u>SEQ. ID NO. 20</u>	AUUUAUUUAUUUA	0.77 +/- 0.25
4c, <u>SEQ. ID NO.21</u>	AUUUAUUUAUUUA	not bound
4d, <u>SEQ. ID NO.22</u>	AUUUAUUUAUUUA	not bound
prel.consensus	NNU/CUNNU/CUU/C	
7a, <u>SEQ. ID NO.23</u>	UAUUUUUUU	not bound
7b, <u>SEQ. ID NO.24</u>	UAUUUUUUU	not bound
7c, <u>SEQ. ID NO.25</u>	UAUUUUUUU	not bound
7d, <u>SEQ. ID NO.26</u>	UAUUUUUUU	not bound
8a, <u>SEQ. ID NO.27</u>	UAUUUUUUU	not bound
8b, <u>SEQ. ID NO.28</u>	UAUUUUUUU	not bound
8c, <u>SEQ. ID NO.29</u>	UAUUUUUUU	not bound
5, <u>SEQ. ID NO.30</u>	UAUUUUUUU	1.14 +/- 0.24
6, <u>SEQ. ID NO.31</u>	AUUUUUUUU	1.01 +/- 0.27
MOTIF	NNUUNUUUU	

Line 7, page 25:

TABLE 1:

Name		Sequence	Position
<i>Openers</i> <u>SEQ.ID NO. 32</u>	O ₁	AATATAAAATTTAAATATTT	804-823
<u>SEQ. ID NO. 33</u>	O ₂	TAGAGCCCCTAGGGCTTACA	909-928
<i>Negative Controls</i> <u>SEQ. ID NO. 34</u>	N ₁	AGTGGAAGCACTTAATTAC	757-775
<u>SEQ. ID NO. 35</u>	N ₂	CATAATAATAAATATTTTGG	969-950

f) Quantitative real-time RT PCR

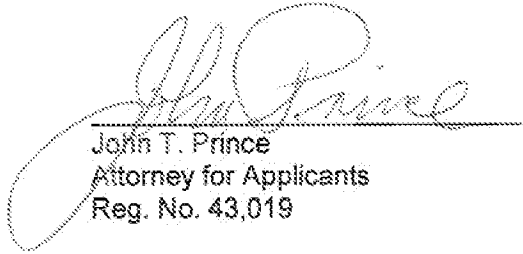
RNA is reverse transcribed to cDNA using the TaqMan RT PCR reagents (Applied Biosystems) and random hexamers for priming following standard protocols. Quantitative RT-PCR is performed with SYBR Green detection on an ABI7700 instrument (Applied Biosystems) with IL-2 specific primers SEQ. ID NO. 36: (forward: 5'-TCACCAGGATGCTCACATTTAAGTT-3'; reverse: 5'-GGAGTTTGAGTTCTTCTTCTAGACACTGA-3'; primers are a gift from F. Kalthoff, Novartis Institute for Biomedical Research Vienna). EF-1 alpha is used as endogenous control for normalization (primers: forward SEQ. ID NO. 37: 5'-TTTGAGACCAGCAAGTACTATGTGACT-3', reverse 5'-TCAGCCTGAGATGTCCCTGTAA -3'). The $\Delta\Delta C_t$ method is used for relative quantification of IL-2 mRNA levels (as described by Applied Biosystems). All presented data are averages from at least 5 identical independent samples and representative of at least two independent experiments using cells from different donors.

Applicant submits that no new material is being added and the amended tables and line amendments bring the specification into conformance with the sequence listing submitted in Response to the Notice of Missing Requirements mailed June 10, 2008.

Respectfully submitted,

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